

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: Abad, et al.
Appl. No.: To Be Assigned
Filed: Concurrently Herewith
For: GENES ENCODING NOVEL PROTEINS WITH PESTICIDAL ACTIVITY
AGAINST COLEOPTERANS

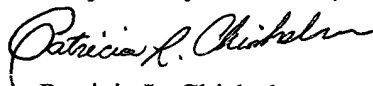
**STATEMENT IN SUPPORT OF FILING A
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Box Patent Application
Commissioner for Patents
Washington, DC 20231

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted concurrently herewith in accordance with 37 CFR § 1.821(c) and (e), are the same.

Respectfully submitted,

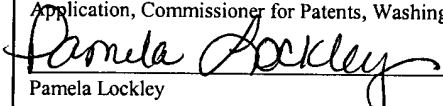


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Pamela Lockley

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner For Patents, Washington, DC 20231, on October 23, 2001.

SEQUENCE LISTING

<110> Andre R. Abad
 Nicholas B. Duck
 Xiang Feng
 Ronald D. Flannagan
 Theodore W. Kahn
 Lynn E. Sims

<120> Genes Encoding Novel Proteins With
 Pesticidal Activity Against Coleopterans

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<151> 2000-10-24

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 Leu Val Ile Pro Asn Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val
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 caa ccg aat caa aga tat gtg tta cga gtt act gcg aga aaa gaa ggg 3264
 Gln Pro Asn Gln Arg Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly
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 Val Gly Asn Gly Tyr Val Ser Ile Arg Asp Gly Gly Asn Gln Thr Glu
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 acg ctt act ttt agt gca agc gat tat gat aca aat gga atg tat aat 3360
 Thr Leu Thr Phe Ser Ala Ser Asp Tyr Asp Thr Asn Gly Met Tyr Asn
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 Thr Gln Val Ser Asn Thr Asn Gly Tyr Asn Thr Asn Asn Ala Tyr Asn
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 Thr Gln Ala Ser Ser Thr Asn Gly Tyr Asn Ala Asn Asn Met Tyr Asn
 1140 1145 1150
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 Thr Gln Ala Ser Asn Thr Asn Gly Tyr Asn Thr Asn Ser Val Tyr Asn
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 Asp Gln Thr Gly Tyr Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr
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 Asp Gln Met Trp Ile Glu Met Ser Glu Thr Glu Gly Thr Phe Tyr Ile
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 Glu Ser Val Glu Leu Ile Val Asp Val Glu *
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 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
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 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
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 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
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 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
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 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
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 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
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 Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
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 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
 225 230 235 240
 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
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 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
 260 265 270
 Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn
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 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
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 Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
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 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
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 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
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 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
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 Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys
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 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
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 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
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 Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
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att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
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Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
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Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln	
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Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
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Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
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ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
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Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp	
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Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
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Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
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aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt gca	1536
Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
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Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala	
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Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro	
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Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
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Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg		255
	260	265
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn		270
	275	280
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg		285
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Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly		300
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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val		315
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Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr		335
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Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala		350
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Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln		365
	370	375
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp		380
	385	390
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu		395
	405	410
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro		415
	420	425
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr		430
	435	440
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp		445
	450	455
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu		460
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Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly		475
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Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala		495
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Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala		510
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Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro		525
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Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser		540
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Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala		555
	565	570
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val		575
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Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr		605
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Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu		620
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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
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Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
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Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
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Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
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Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp	
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Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
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Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Trp Lys Glu Asn Pro	
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Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
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Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	
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Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu	
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Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys		
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Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg		
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Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn		
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Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg		
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Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala		
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Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu		
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ctt	gat	att	gtt	ttt	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Phe	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro		
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gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr			
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Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Gln	Lys	Ser	Gln	Trp
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Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu
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Ser	Glu	Leu	Glu	Leu	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu	
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Ser	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala
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Asp	Leu	Ile	Asn	Ala	Val	His	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Val
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Val	Lys	Val	Ser	Asp	Leu	Ala	Pro	Ser	Ile	Thr	Gly	Gly	Pro	Asn	Asn

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 Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala
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 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
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 tcc gcc ggc aac gcc tcc gag tac ccc ggc tcc ccc gag gtg ctc gtg 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 tcc ggc cag gac gcc gcc aag gcc gcc atc gac atc gtg ggc aag ctc 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 ctc tcc ggc ctc ggc gtg ccc ttc gtg ggc ccc atc gtg tcc ctc tac 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 acc cag ctc atc gac atc ctc tgg ccc tcc ggc gag aag tcc cag tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110

gaa atc ttc atg gag cag gtg gag gag ctc atc aac cag aag atc gcc	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gag tac gcc cgc aac aag gcc ctc tcc gag ctg gag ggc ctc ggc aac	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aac tac cag ctc tac ctc acc gcc ctg gag gag tgg gag gag aac ccc	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aac ggc tcc cgc gcc ctc cgc gac gtg cgc aac cgc ttc gag atc ctc	528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
165 170 175	
gac tcc ctc ttc acc cag tac atg ccc tcc ttc cgc gtg acc aac ttc	576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	
180 185 190	
gag gtg ccc ttc ctc acc gtg tac gcc atg gcc gcc aac ctc cac ctc	624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu	
195 200 205	
ctc ctc ctc aag gac gcc tcc atc ttc ggc gag gag tgg ggc tgg tcc	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
acc acc acc atc aac aac tac tac gac cgc cag atg aag ctc acc gcc	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gag tac tcc gac cac tgc gtg aag tgg tat gag acc ggc ctc gcc aag	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
ctc aag ggc acc tcc gcc aag cag tgg gtg gac tac aac cag ttc cgc	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
cgc gag atg acc ctc gcc gtg ctc gac gtg gtg gcc ctc ttc ccc aac	864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tac gac acc cgc acc tac ccc atg gag acc aag gcc cag ctc acc cgc	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gag gtg tac acc gac ccg ctc ggc gcc gtg aac gtg tcc tcc atc ggc	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tct tgg tac gac aag gcc cca agc ttc ggc gtg atc gag tcc tcc gtg	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
atc cgc ccg ccg cac gtg ttc gac tac atc acc ggc ctc acc gtg tac	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
acc cag tcc cgc tcc atc tcc tcc gcc cgc tac atc cgc cac tgg gcc	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	

610	615	620	
acc ctc aac ctc gcc acc gac tcc tcc ctc gcc ctc aag cac aac ctc			1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu			
625	630	635	640
ggc gag gac ccc aac tcc acc ctc tcc ggc atc gtg tac gtg gac cgc			1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg			
645	650	655	
atc gag ttc atc ccc gtg gac gag acc tac gag gcc gag tga			2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *			
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Maize optimized Cry1218-1

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 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
 165 170 175
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
 180 185 190
 Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu
 195 200 205
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser
 210 215 220
 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
 225 230 235 240
 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
 245 250 255
 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
 260 265 270
 Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn
 275 280 285
 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
 290 295 300

Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
 305 310 315 320
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
 325 330 335
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
 340 345 350
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
 355 360 365
 Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln
 370 375 380
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
 385 390 395 400
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
 405 410 415
 Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
 420 425 430
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
 435 440 445
 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp
 450 455 460
 Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu
 465 470 475 480
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly
 485 490 495
 Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala
 500 505 510
 Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala
 515 520 525
 Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro
 530 535 540
 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser
 545 550 555 560
 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala
 565 570 575
 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val
 580 585 590
 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro
 595 600 605
 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr
 610 615 620
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu
 625 630 635 640
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg
 645 650 655
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu
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<210> 11
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<221> misc_feature
 <222> (0)...(0)
 <223> NGSR.N1218-1

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1				5					10					15		
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu	
			20					25				30				
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met	
		35					40				45					
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val	
	50					55					60					
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	
	65				70				75						80	
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	
			85					90						95		
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	
			100					105					110			
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala	
		115					120					125				
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	
	130					135					140					
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	
	145				150				155					160		
aat	ggg	tca	aga	aat	ggg	tcc	cgg	gcc	tta	cga	gat	gtg	cga	aat	cga	528
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	
			165					170					175			
ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	576
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	
		180						185					190			
gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	624
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	
		195					200					205				
aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	672
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	
	210					215					220					
tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	720
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	
	225				230					235				240		
aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	768
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	
			245					250						255		

ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	

	85		90		95										
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
	100							105						110	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
	115						120							125	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
	145				150					155					160
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg
				165						170				175	
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg
			180					185					190		
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala
	195						200					205			
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
	210				215							220			
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
	225				230					235					240
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
			245						250					255	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
		260					265						270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
	275					280						285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala
	290				295					300					
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
	305				310					315					320
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
			325					330						335	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
		340					345						350		
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile
	355					360						365			
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly
	370				375					380					
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr
	385				390				395						400
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys
			405						410					415	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe
		420					425						430		
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn
	435					440					445				
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala
	450				455						460				
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln
	465				470				475						480
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile
			485					490					495		
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr
	500						505						510		
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr
	515					520						525			
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val
	530				535						540				
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg
	545				550				555						560
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala
			565					570						575	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp
	580						585						590		

Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
595 600 605
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
610 615 620
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu
625 630 635 640
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
645 650 655
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
660 665 670
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<210> 13
<211> 12
<212> DNA
<213> Artificial Sequence

<220>

<223> NGS Insert

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<210> 14
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> NGS Insert

<400> 14
Asn Gly Ser Arg
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<210> 15
<211> 2010
<212> DNA
<213> Bacillus thuringiensis (truncated)

<220>

<221> CDS

<222> (1)...(2010)

<221> misc_feature

<222> (0)...(0)

<223> 1218-1A

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met

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tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt			192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val			
50	55	60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta			240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu			
65	70	75	80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat			288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr			
85	90	95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg			336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp			
100	105	110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca			384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala			
115	120	125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat			432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg			528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu			
165	170	175	
gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat ttt			576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe			
180	185	190	
gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat tta			624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu			
195	200	205	
ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg tca			672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser			
210	215	220	
aca act act att aat aac tat tat gat cgt caa atg aaa ctt act gca			720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala			
225	230	235	240
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa			768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys			
245	250	255	
tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc cgt			816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg			
260	265	270	
aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca aat			864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn			
275	280	285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg			912

gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
545 550 555 560	
gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa gca	1728
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala	
565 570 575	
ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att gta	1776
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val	
580 585 590	
ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca	1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro	
595 600 605	
ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca	1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr	
610 615 620	
aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta	1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu	
625 630 635 640	
ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga	1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg	
645 650 655	
atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa	2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *	
660 665	

<210> 16
 <211> 669
 <212> PRT
 <213> *Bacillus thuringiensis* (truncated)

<400> 16

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
165 170 175	
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	

<210> 17
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (truncated)

<220>
 <221> CDS
 <222> (1)...(2022)

<221> misc_feature
 <222> (0)...(0)
 <223> 1218-2A

<400> 17
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
 100 105 110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
 145 150 155 160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
 165 170 175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
 180 185 190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624

Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu	
195 200 205	
ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
aca acc act att aat aac tat tat gat cgt caa atg aaa ctt act gca	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
tta aaa ggc acg agc gct aaa caa tgg gtc gac tat aac caa ttc cgt	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
aga gaa atg aca ctg acg gtt tta gat gtt gtt gca tta ttc cca aat	864
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	
ggt cat caa ata agc tat cat cgg att ttt agt gat aat att ata aaa	1152
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
370 375 380	
cag atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag acg tta tca aaa gat gcg gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt ttt cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	

<212> PRT

<213> Bacillus thuringiensis (truncated)

<400> 18

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
145 150 155 160
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165 170 175
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
180 185 190
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
195 200 205
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser
210 215 220
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
225 230 235 240
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
245 250 255
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
260 265 270
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn
275 280 285
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
290 295 300
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
305 310 315 320
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
325 330 335
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
340 345 350
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
355 360 365
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys
370 375 380
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
385 390 395 400
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
405 410 415
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
420 425 430
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
435 440 445
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp
450 455 460
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu

aat ctt caa caa atg tat gga act aat caa aat cta cac agc act agt 1059
Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser
335 340 345 350

acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat 1107
Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp
355 360 365

gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt 1155
Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe
370 375 380

gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc 1203
Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr
385 390 395

aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt 1251
Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser
400 405 410

aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca 1299
Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro
415 420 425 430

aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc 1347
Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro
435 440 445

gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat 1395
Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His
450 455 460

cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa 1443
Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln
465 470 475

att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta 1491
Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val
480 485 490

aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt 1539
Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser
495 500 505 510

act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta 1587
Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu
515 520 525

gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca 1635
Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala
530 535 540

gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca 1683
Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr
545 550 555

atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat 1731
Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp
560 565 570

gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa 1779
Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys

575 580 585 590

cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac 1827
 His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr
 595 600 605

gtt gac cga atc gaa ttc atc cca gta gat taa 1860
 Val Asp Arg Ile Glu Phe Ile Pro Val Asp *
 610 615

<210> 20
 <211> 616
 <212> PRT
 <213> Bacillus thuringiensis (truncated)

<400> 20
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110
 Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile
 115 120 125
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn
 130 135 140
 Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His
 145 150 155 160
 Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp
 165 170 175
 Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr
 180 185 190
 Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala
 195 200 205
 Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe
 210 215 220
 Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro
 225 230 235 240
 Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr
 245 250 255
 Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile
 260 265 270
 Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser
 275 280 285
 Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val
 290 295 300
 Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp
 305 310 315 320
 Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu
 325 330 335
 Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe
 340 345 350
 Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val
 355 360 365

100327-100303

Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met
 370 375 380
 Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys
 385 390 395 400
 Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg
 405 410 415
 Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr
 420 425 430
 Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr
 435 440 445
 Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser
 450 455 460
 Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro
 465 470 475 480
 Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly
 485 490 495
 Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly
 500 505 510
 Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys
 515 520 525
 Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile
 530 535 540
 Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn
 545 550 555 560
 Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile
 565 570 575
 Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn
 580 585 590
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp
 595 600 605
 Arg Ile Glu Phe Ile Pro Val Asp
 610 615

<210> 21
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)
 <221> misc_feature
 <222> (0)...(0)
 <223> LKMS.N1218-1

<400> 21
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 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Glu Val Leu Val
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aaa atg tct aat ggt tca aga gcc tta cga gat gtg cga aat cga	528
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	

Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575

tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat 1776
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590

gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa 1824
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605

aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca 1872
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620

gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg 1920
 Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu
 625 630 635 640

aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt 1968
 Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670

gaa taa
 Glu * 2022

<210> 22

<211> 673

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 22

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
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 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg
 165 170 175
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<210> 23
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 <222> (1)...(2013)

<221> misc_feature
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Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
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tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
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agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
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cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc	528
Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile	
165 170 175	
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Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn	
180 185 190	
ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat	624

Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
195 200 205	
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Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
210 215 220	
tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt act	720
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
225 230 235 240	
gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca	768
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
245 250 255	
aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc	816
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	
260 265 270	
cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca	864
Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro	
275 280 285	
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Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr	
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Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile	
305 310 315 320	
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Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser	
325 330 335	
gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg	1056
Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val	
340 345 350	
tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg	1104
Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp	
355 360 365	
gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt	1152
Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu	
370 375 380	
caa caa atg tat gga act aat caa aat cta cac agc act agt acc ttt	1200
Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe	
385 390 395 400	
gat ttt acg aat tat gat att tac aag act cta tca aag gat gca gta	1248
Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val	
405 410 415	
ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg	1296
Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met	
420 425 430	
cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag	1344
Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys	
435 440 445	

Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser
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 Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro
 515 520 525
 Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly
 530 535 540
 Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly
 545 550 555 560
 Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys
 565 570 575
 Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile
 580 585 590
 Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn
 595 600 605
 Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile
 610 615 620
 Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn
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<220>

<223> LKMS Insert

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<210> 26
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>

<223> LKMS Insert

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<210> 27
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 <212> DNA
 <213> Bacillus thuringiensis

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 tgtgggcaaa ttgagataga tttacatgct ttaaaaatta aaggtgtttt accgtttatc 180


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tcaaacagaa acgcttactt ttagtgcaag cgattatgat acaaatggaa tgtataatac 4080
gcaagtgtcc aatacaaatg gatataacac aaataatgcg tataatacac aagcatcgag 4140
tacaacgga tataacgcaa ataatatgta taatacgcaa gcatcgaaata caaacggata 4200
taacacaaat agtgtgtaca atgatcaaac cggctatata aaaaaacag tgacattcat 4260
cccgtatata gatcaaatgt ggattgagat gaggtagaca gaaggtagat tctatataga 4320
aagtgtagaa ttgattgtag acgtagagta atagtagtac cctccagat gaaacctgta 4380
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attacatatt ttgtgaatag gactatggtt gggtacctta cggtagcttt ttatatccac 4500
cggcattgga aaatgtaaga gggaggataa tcatatatag tcccttccct acacatcaaa 4560
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gatatttgta ataatacaagt catagttttt tgcaatctgt ttaaatgagc tgagatgtaa 4740
tacaatcaatc ttagatagtt gaatcatatg accaaattga tactgcataa tattacgaat 4800
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4874

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<210> 28
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<212> DNA
<213> Bacillus thuringiensis

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<223> Genomic Cry1218-2

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tgtacgaggt cgaattgacg taacagggca cctttttggt caaattgacc aaagaatcca 180
tcctttgcat gagcacttct cgaaaccact tcccatagtg cacttcttat cttttgtata 240
tatttcctaa ggatatacgt atccctatct ctgataagag gattttgtca gtgtaggaa 300
agcgaatgtc ttttcgtatt tcaaacaaaa aataaaggat gtttatgcac ggaaataatc 360
atcatattaa taatgcccgac tacataaaga tagatggggg tcattttttg aaatgattcg 420
aaaagactcc gttgactcga taggaggtgc acagaaaaat ggaagaaaga tatgcatcgc 480
aagatcagtc ggtatgtaga gtttctaata gcaaggggaa gaaaaacccat acagttccct 540
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cgtttatcgt gaacgtatcc attgaaccgc ttagtatgaa catgtatata ccacaagtgg 780
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ttaaaaaaag tgtaagaaat tttatatctt ttgtatgtat aggaggaaaa tagatgagtc 1260
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gttttagggg cccatttgtt gggccgatag tgagtcctta tactcaactt attgatattc 1560
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cagccaacct tcatttactg ttattaaagg acgcttcaat ttttgagaa gaatggggat 1920
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ctgatcactg tgtaaagtgg tatgaaactg gtttagcaaa attaaaaggc acgagcgcta 2040
aacaatgggt cgactataac caattccgta gagaaatgac actgacgggt ttgatgttg 2100

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<210> 29
<211> 1863
<212> DNA
<213> Bacillus thuringiensis (mutated)

<220>
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<222> (1)...(1863)
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<223> NGS.R.N49PVD

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ggt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96
Val Ser Gly Gln Asp Ala Ala Lys Ala Ile Asp Ile Val Gly Lys
20 25 30
tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
35 40 45
tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
50 55 60
tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
65 70 75 80
gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
85 90 95
aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
100 105 110
cca aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat 384
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
115 120 125
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt 432

Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
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aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	480
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
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Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
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Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
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Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
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Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
290 295 300	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	960
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
305 310 315 320	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1008
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
325 330 335	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1056
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
340 345 350	
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1104
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
355 360 365	
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1152
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	

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385 390 395 400	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
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Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
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aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1440
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
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Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
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Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
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Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
545 550 555 560	
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Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
565 570 575	
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580 585 590	
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
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<210> 30
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<212> PRT

<213> *Bacillus thuringiensis* (mutated)

<400> 30

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35 40 45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
50 55 60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
65 70 75 80
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
85 90 95
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
100 105 110
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
115 120 125
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130 135 140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
145 150 155 160
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
165 170 175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
180 185 190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
195 200 205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
210 215 220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
225 230 235 240
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
245 250 255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
260 265 270
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
275 280 285
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
290 295 300
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
305 310 315 320
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
325 330 335
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
340 345 350
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
355 360 365
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
370 375 380
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
385 390 395 400
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
405 410 415
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
420 425 430
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
435 440 445
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
450 455 460
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile

aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1152
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1200
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
385 390 395 400	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1392
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
450 455 460	
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1440
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
465 470 475 480	
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1488
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
485 490 495	
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1536
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
500 505 510	
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1584
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
515 520 525	
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1632
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
530 535 540	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1680
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
545 550 555 560	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
565 570 575	
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca	1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala	
580 585 590	
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
595 600 605	
gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa	1863
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *	

610

615

620

<210> 32
 <211> 620
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 32

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ile Asp Ile Val Gly Lys
 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110
 Pro Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
 115 120 125
 Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
 130 135 140
 Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
 145 150 155 160
 Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
 165 170 175
 Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
 180 185 190
 Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
 195 200 205
 Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
 210 215 220
 Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
 225 230 235 240
 Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
 245 250 255
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
 260 265 270
 Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
 275 280 285
 Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
 290 295 300
 Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
 305 310 315 320
 Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
 325 330 335
 Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
 340 345 350
 Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
 355 360 365
 Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
 370 375 380
 Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
 385 390 395 400
 Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
 405 410 415
 Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
 420 425 430

Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
 435 440 445
 Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
 450 455 460
 Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile
 465 470 475 480
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro
 485 490 495
 Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn
 500 505 510
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu
 515 520 525
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr
 530 535 540
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
 545 550 555 560
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
 580 585 590
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
 595 600 605
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp
 610 615 620

<210> 33
 <211> 1854
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(1854)
 <221> misc_feature
 <222> (0)...(0)
 <223> LKMS.R49PVD

<400> 33
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 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95

aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat	336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
cca tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa	384
Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu	
115 120 125	
atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca	432
Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr	
130 135 140	
aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt	480
Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu	
145 150 155 160	
cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga	528
His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly	
165 170 175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt	576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu	
180 185 190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta	624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu	
195 200 205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa	672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln	
210 215 220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc	720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe	
225 230 235 240	
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta	768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu	
245 250 255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca	816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser	
260 265 270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca	864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser	
275 280 285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca	912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr	
290 295 300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat	960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His	
305 310 315 320	
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat	1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn	
325 330 335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc	1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr	

340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala 355 360 365			1104
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly 370 375 380			1152
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg 385 390 395 400			1200
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr 405 410 415			1248
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn 420 425 430			1296
tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala 435 440 445			1344
acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg 450 455 460			1392
agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa att Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile 465 470 475 480			1440
ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys 485 490 495			1488
gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr 500 505 510			1536
ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu 515 520 525			1584
aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp 530 535 540			1632
att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met 545 550 555 560			1680
aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala 565 570 575			1728
atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His 580 585 590			1776
aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt			1824

Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val
 595 600 605

gac cga atc gaa ttc atc cca gta gat taa
 Asp Arg Ile Glu Phe Ile Pro Val Asp *
 610 615

1854

<210> 34
 <211> 617
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 34

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110
 Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu
 115 120 125
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr
 130 135 140
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu
 145 150 155 160
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly
 165 170 175
 Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu
 180 185 190
 Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu
 195 200 205
 Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln
 210 215 220
 Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe
 225 230 235 240
 Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu
 245 250 255
 Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser
 260 265 270
 Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser
 275 280 285
 Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr
 290 295 300
 Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His
 305 310 315 320
 Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn
 325 330 335
 Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr
 340 345 350
 Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala
 355 360 365
 Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly
 370 375 380
 Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg

385 390 395 400
 Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr
 405 410 415
 Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn
 420 425 430
 Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala
 435 440 445
 Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg
 450 455 460
 Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile
 465 470 475 480
 Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys
 485 490 495
 Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr
 500 505 510
 Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu
 515 520 525
 Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp
 530 535 540
 Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met
 545 550 555 560
 Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala
 565 570 575
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His
 580 585 590
 Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val
 595 600 605
 Asp Arg Ile Glu Phe Ile Pro Val Asp
 610 615

<210> 35
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' forward primer

<400> 35
 atgagtccaa ataatacaaaa tg

22

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' reverse primer

<400> 36
 ccgcttctaa atcttgttcc

20

<210> 37
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' forward primer

<400> 37
 ggaacaagat ttagagg

17

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' reverse primer

<400> 38
 ctcacgtct acaatcaatt catc 24

<210> 39
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)
 <221> misc_feature
 <222> (0)...(0)
 <223> LRNS.N1218-1

<400> 39
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Gly Leu Gly Asn
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480

agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys 405 410 415	1248
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe 420 425 430	1296
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn 435 440 445	1344
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala 450 455 460	1392
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln 465 470 475 480	1440
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile 485 490 495	1488
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr 500 505 510	1536
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr 515 520 525	1584
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val 530 535 540	1632
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg 545 550 555 560	1680
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala 565 570 575	1728
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp 580 585 590	1776
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys 595 600 605	1824
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala 610 615 620	1872
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu 625 630 635 640	1920
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val 645 650 655	1968

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670

gaa taa
 Glu * 2022

<210> 40
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 40
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg
 165 170 175
 Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg
 180 185 190
 Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala
 195 200 205
 Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu
 210 215 220
 Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met
 225 230 235 240
 Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr
 245 250 255
 Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr
 260 265 270
 Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala
 275 280 285
 Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala
 290 295 300
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
 305 310 315 320
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
 325 330 335
 Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
 340 345 350
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly

tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt	144
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu	
35 40 45	
tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa	192
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln	
50 55 60	
tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata	240
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile	
65 70 75 80	
gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt	288
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly	
85 90 95	
aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat	336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
cca tta aga atg tct aat ggt tcc cgg gcc tta cga gat gtg cga aat	384
Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn	
115 120 125	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	432
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
130 135 140	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	480
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	

ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr 290 295 300	912
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr 305 310 315 320	960
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg 325 330 335	1008
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser 340 345 350	1056
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser 355 360 365	1104
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile 370 375 380	1152
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn 385 390 395 400	1200
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile 405 410 415	1248
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp 420 425 430	1296
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser 435 440 445	1344
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp 450 455 460	1392
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile 465 470 475 480	1440
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro 485 490 495	1488
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn 500 505 510	1536
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu 515 520 525	1584
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	1632

530

535

540

gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca 1680
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
 545 550 555 560

aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt 1728
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575

gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca 1776
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
 580 585 590

ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata 1824
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
 595 600 605

gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa 1863
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *
 610 615 620

<210> 42

<211> 620

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 42

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110
 Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
 115 120 125
 Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
 130 135 140
 Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
 145 150 155 160
 Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
 165 170 175
 Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
 180 185 190
 Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
 195 200 205
 Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
 210 215 220
 Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
 225 230 235 240
 Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
 245 250 255
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
 260 265 270

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc	528
Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile	
165 170 175	
ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat	576
Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn	
180 185 190	
ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat	624
Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
195 200 205	
tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg	672
Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
210 215 220	
tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt act	720
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
225 230 235 240	
gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca	768
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
245 250 255	
aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc	816
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	

Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro
515 520 525

gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga 1632
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly
530 535 540

cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt 1680
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly
545 550 555 560

tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa 1728
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys
565 570 575

gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att 1776
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile
580 585 590

gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac 1824
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn
595 600 605

cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc 1872
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile
610 615 620

aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat 1920
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn
625 630 635 640

tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac 1968
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp
645 650 655

cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa 2013
Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *
660 665 670

<210> 44
<211> 670
<212> PRT
<213> Bacillus thuringiensis (mutated)

<400> 44
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125

Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile
 165 170 175
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn
 180 185 190
 Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His
 195 200 205
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp
 210 215 220
 Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr
 225 230 235 240
 Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala
 245 250 255
 Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe
 260 265 270
 Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro
 275 280 285
 Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr
 290 295 300
 Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile
 305 310 315 320
 Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser
 325 330 335
 Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val
 340 345 350
 Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp
 355 360 365
 Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu
 370 375 380
 Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe
 385 390 395 400
 Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val
 405 410 415
 Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met
 420 425 430
 Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys
 435 440 445
 Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg
 450 455 460
 Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr
 465 470 475 480
 Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr
 485 490 495
 Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser
 500 505 510
 Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro
 515 520 525
 Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly
 530 535 540
 Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly
 545 550 555 560
 Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys
 565 570 575
 Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile
 580 585 590
 Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn
 595 600 605
 Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile
 610 615 620
 Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn

625 630 635 640
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp
 645 650 655
 Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu
 660 665 670

<210> 45
 <211> 1854
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(1854)

<221> misc_feature
 <222> (0)...(0)
 <223> LRMS.R49PVD

<400> 45
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 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15

 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30

 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45

 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60

 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80

 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95

 aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110

 cca tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa 384
 Pro Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu
 115 120 125

 atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca 432
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr
 130 135 140

 aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt 480
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu
 145 150 155 160

 cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga 528
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly

165	170	175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt			576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu			
180	185	190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta			624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu			
195	200	205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa			672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln			
210	215	220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc			720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe			
225	230	235	240
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta			768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu			
245	250	255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca			816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser			
260	265	270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca			864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser			
275	280	285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca			912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr			
290	295	300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat			960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His			
305	310	315	320
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat			1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn			
325	330	335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc			1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr			
340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca			1104
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala			
355	360	365	
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga			1152
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly			
370	375	380	
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga			1200
Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg			
385	390	395	400
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca			1248
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr			
405	410	415	
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat			1296

Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn	
420 425 430	
tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg	1344
Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala	
435 440 445	
acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga	1392
Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg	
450 455 460	
agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa att	1440
Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile	
465 470 475 480	
ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa	1488
Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys	
485 490 495	
gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act	1536
Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr	
500 505 510	
ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa	1584
Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu	
515 520 525	
aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat	1632
Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp	
530 535 540	
att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg	1680
Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met	
545 550 555 560	
aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct	1728
Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala	
565 570 575	
atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat	1776
Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His	
580 585 590	
aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt	1824
Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val	
595 600 605	
gac cga atc gaa ttc atc cca gta gat taa	1854
Asp Arg Ile Glu Phe Ile Pro Val Asp *	
610 615	

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 <211> 617
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 46
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
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 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
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 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu

35	40	45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln		
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Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile		
65	70	75
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly		80
	85	90
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn		95
	100	105
Pro Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu		110
	115	120
Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr		125
	130	135
Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu		140
145	150	155
His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly		160
	165	170
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu		175
	180	185
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu		190
	195	200
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln		205
	210	215
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe		220
225	230	235
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu		240
	245	250
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser		255
	260	265
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser		270
	275	280
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr		285
	290	295
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His		300
305	310	315
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn		320
	325	330
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr		335
	340	345
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala		350
	355	360
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly		365
	370	375
Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg		380
385	390	395
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr		400
	405	410
Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn		415
	420	425
Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala		430
	435	440
Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg		445
	450	455
Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile		460
465	470	475
Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys		480
	485	490
Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr		495
	500	505
Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu		510
	515	520
Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp		525
	530	535
		540

Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met
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Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala
				565					570						575
Ile	Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His
			580					585						590	
Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	Tyr	Val
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	610					615									

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<220>

<223> LRMS Insert

<400> 47
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<220>

<223> LRMS Insert

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